



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

reinforcing the need for continuous measures to contain SARS-CoV-2 spread, despite growing pandemic fatigue in the population,<sup>5</sup> and to avoid potentially catastrophic COVID-19-related hospitalisations and deaths in the critical months ahead.

We declare no competing interests.

\*Silvia Stringhini, María-Eugenia Zaballa, Javier Perez-Saez, Nick Pullen, Carlos de Mestral, Attilio Picazio, Francesco Pennacchio, Ania Wisniak, Aude Richard, Helene Baysson, Andrea Loizeau, Jean-François Balavoine, Didier Trono, Didier Pittet, Klara Posfay-Barbe, Antoine Flahault, François Chappuis, Omar Kherad, Nicolas Vuilleumier, Laurent Kaiser, Andrew S Azman, Idris Guessous, for the Specchio-COVID19 Study Group† silvia.stringhini@hcuge.ch

†Group members are listed in the appendix (p 5)

Division of Primary Care Medicine (SS, M-EZ, NP, CdM, AP, FP, AW, AR, HB, AL, ASA, IG), Infection Control Program and WHO Collaborating Centre on Patient Safety (DP), Division of General Pediatrics (KP-B), Division of Tropical and Humanitarian Medicine (FC), Division of Laboratory Medicine (NV), and Geneva Center for Emerging Viral Diseases (LK), Geneva University Hospitals, Geneva, Switzerland; Faculty of Medicine, University of Geneva, Switzerland (SS, AR, HB, AL, J-FB, DP, KP-B, AF, FC, OK, NV, LK, IG); Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA (JP-S, ASA); School of Life Sciences, Ecole Polytechnique Fédérale de Lausanne, Lausanne, Switzerland (DT); Division of Internal Medicine, Hôpital de la Tour, Geneva, Switzerland (OK)

- 1 Johns Hopkins University & Medicine. New cases of COVID-19 in world countries. <https://coronavirus.jhu.edu/data/new-cases> (accessed Jan 8, 2021).
- 2 Stringhini S, Wisniak A, Piumatti G, et al. Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Geneva, Switzerland (SEROCoV-POP): a population-based study. *Lancet* 2020; **396**: 313–19.
- 3 Bonanad C, García-Blas S, Tarazona-Santabalbina F, et al. The effect of age on mortality in patients with Covid-19: a meta-analysis with 611 583 subjects. *J Am Med Dir Assoc* 2020; **21**: 915–18.
- 4 Yanez ND, Weiss NS, Romand J-A, Treggiari MM. COVID-19 mortality risk for older men and women. *BMC Public Health* 2020; **20**: 1742.
- 5 World Health Organization Regional Office for Europe. Pandemic fatigue: reinvigorating the public to prevent COVID-19. <https://apps.who.int/iris/bitstream/handle/10665/337574/WHO-EURO-2020-1573-41324-56242-eng.pdf> (accessed Dec 18, 2020).

## Long COVID: tackling a multifaceted condition requires a multi-disciplinary approach

In their Comment,<sup>1</sup> Dana Yelin and colleagues highlight the persistent, heterogeneous, and recurring symptoms of long COVID. A *Lancet* Editorial<sup>2</sup> asks for better research and care to avoid years of struggle for individuals with long COVID. We write following an international, multi-stakeholder forum, in which peoples' voices were central, to expand the call to action and to identify how we can prevent long COVID from becoming the long-lasting legacy of COVID-19.

On Dec 9–10, 2020, the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC), the Global Research Collaboration for Infectious Disease Preparedness (GloPID-R) research funders group, and Long COVID Support, a global patient group, held the Long COVID Forum (appendix pp 1–2). We brought together people living with long COVID, interdisciplinary researchers, funders, public health experts, and policy makers, including WHO, in a global public forum to identify research gaps to inform urgent long COVID research and support priorities.

Our discussions, introduced by WHO Director-General Tedros Adhanom Ghebreyesus, were built around three people-centred themes, identified by long COVID support groups: recognition, research, and rehabilitation. We heard from people living with long COVID from around the world, who asked: what is causing my illness? What can I do to recover? Why do I have long COVID when others recover quickly? How do I convince my doctor that what I am suffering from is real? How can others be prevented from getting long COVID? We explored existing evidence,<sup>3</sup> including the recently funded research portfolio on long COVID that will contribute to the evidence body in the short to

mid-term<sup>4</sup> and updates from ongoing research from around the world. A complex, multifaceted condition involving a range of physical, cognitive, and psychological symptoms was described, affecting adults and children in different settings, with occupational, economic, and social implications. Such complexity requires a multi-disciplinary, globally coordinated approach that supports harmonised, large-scale studies that have the power to provide robust evidence to inform policy and patient-centred care and support to improve long COVID outcomes.

The structure of the forum facilitated the identification of research gaps (appendix p 3). The core message was the need to expand research beyond hospitalised patients to include those who experienced COVID-19 in the community, children, vulnerable communities, and resource-constrained populations to improve equity in access to research and reduce health inequalities.

CH is living with long COVID and is a founder of the Long Covid Support Group. JCS reports experiencing persisting symptoms of COVID-19, following suspected COVID-19 in March, 2020. All other authors declare no competing interests.

Alice Norton, \*Piero Olliaro, Louise Sigfrid, Gail Carson, Giuseppe Paparella, Claire Hastie, Charu Kaushic, Geneviève Boily-Larouche, Jake C Suett, Margaret O'Hara, on behalf of the ISARIC and GloPID-R Long COVID Forum Working Group† piero.olliaro@ndm.ox.ac.uk

UK Collaborative on Development Research, London, UK (AN); ISARIC Global Support Centre, Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford OX3 7FZ, UK (PO, LS, GC, GP); Long Covid Support, UK (CH, MO'H); McMaster Immunology Research Centre and Department of Medicine, McMaster University, Hamilton, ON, Canada (CK); Institute of Infection and Immunity Canadian Institutes of Health Research, Government of Canada, Ottawa, ON, Canada (GB-L); Queen Elizabeth Hospital, King's Lynn, UK (JCS)

†Group members are listed in the appendix (p 1)

- 1 Yelin D, Wirtheim E, Vetter P, et al. Long-term consequences of COVID-19: research needs. *Lancet Infect Dis* 2020; **20**: 1115–17.
- 2 The Lancet. Facing up to long COVID. *Lancet* 2020; **396**: 1861.



Published Online  
February 3, 2021  
[https://doi.org/10.1016/S1473-3099\(21\)00043-8](https://doi.org/10.1016/S1473-3099(21)00043-8)  
This online publication has been corrected. The corrected version first appeared at [thelancet.com/infection](https://www.thelancet.com/infection) on February 16, 2021

See Online for appendix



Published Online  
February 8, 2021  
[https://doi.org/10.1016/S1473-3099\(21\)00078-5](https://doi.org/10.1016/S1473-3099(21)00078-5)

This online publication has been corrected. The corrected version first appeared at [thelancet.com/infection](http://thelancet.com/infection) on March 1, 2021

## CovMT: an interactive SARS-CoV-2 mutation tracker, with a focus on critical variants

The number of confirmed SARS-CoV-2 cases worldwide has now reached around 100 million, with 2.1 million reported deaths<sup>1</sup> and more than 450 000 SARS-CoV-2 genomes already sequenced. It is vital to keep track of mutations in the genome of SARS-CoV-2, especially in the spike protein's receptor binding domain (RBD) region, which could potentially impact disease severity and treatment strategies.<sup>2-4</sup> In the wake of a recent increase in cases with a more infective variant featuring an RBD mutation (N501Y, B.1.1.7) in the UK, countries worldwide are concerned about the spread of this or similar variants. Increasing sequencing efforts and user-friendly mutation tracking systems are needed for timely tracking of SARS-CoV-2 variants.

We developed a COVID-19 virus mutation tracker system (CovMT; appendix) based on SARS-CoV-2 isolate genomes deposited to GISAID to track the worldwide sequencing efforts and the evolution of the mutational landscape of this virus. CovMT, which is updated daily, summarises mutations from more than 450 000 isolates into groups of generic virus clades, lineages, and more specific mutation sets we call mutation fingerprints. These summaries, with metadata of location, date of sampling, and patient disease severity information, when available, at the continent and country levels, are accessible from the main page of the CovMT system (appendix).

CovMT also provides a timeline history of SARS-CoV-2 variants related to mutations in the RBD region of the spike protein. As of the end of January, 2021, the spread of N501Y, B.1.1.7 variants has been detected in SARS-CoV-2 isolate genomes from nearly 60 additional countries using CovMT (appendix). Nonsynonymous mutations in the RBD region have a high potential to be linked to increased binding efficiency, increased infectivity, and the potential to evade antibodies.<sup>2-4</sup> To track all similar variants, we ranked mutations in the RBD region based on their appearance in the number of isolate genomes in CovMT. The CovMT timeline (appendix) shows that N501Y, S477N, N439K, and L452R mutations can now be detected in more than 41 700, 23 300, 9700, and 2000 isolates, respectively. An important RBD mutation, E484K, which probably allows the virus to evade existing antibodies,<sup>5</sup> was originally recorded in Denmark during March, 2020, and is now on the rise in South Africa<sup>5</sup> since October, 2020. More than 510 isolates show triple mutations (K417N, E484K, and N501Y, lineage B.1.351) in South Africa, with some isolates now detected in the UK and 22 other countries. We observed that the UK variant (B.1.1.7) has also acquired the E484K mutation (appendix). A more recent variant, P.1, with E484K and N501Y RBD mutations, appeared in four travellers arriving in Japan from Brazil on Jan 2, 2021. The P.1 variant now appears in six other countries. Timelines and lineage history of each of the top ten most common RBD mutations can be explored at CovMT.

With a particular focus on critical mutations in the RBD region of the spike protein, and with an option to seamlessly accrue the clinical metadata, including disease severity, we believe that CovMT will be useful for scientists, the general public, and authorities to explore country-specific information.

We declare no competing interests. We are thankful to King Abdullah University of Science and Technology information technology and supercomputing laboratory teams for maintaining the computational resources and helping to publish the CovMT website, and to GISAID for providing daily updates on sequenced isolates worldwide. This work is supported by King Abdulaziz City of Science and Technology grant for COVID-19 research, number 0004-002-01-20-5.

\*Intikhab Alam, Aleksandar Radovanovic, Roberto Incitti, Allan A Kamau, Mohammed Alarawi, Esam I Azhar, Takashi Gojobori  
[intikhab.alam@kaust.edu.sa](mailto:intikhab.alam@kaust.edu.sa)

Computational Bioscience Research Center, King Abdullah University of Science and Technology, Thuwal, Makkah, Saudi Arabia (IA, AR, RI, AAK, MA, TG); Special Infectious Agent Unit, King Fahd Medical Research Center, and Medical Laboratory Technology Department, Faculty of Applied Medical Sciences, King Abdulaziz University, Jeddah, Saudi Arabia (EIA)

- 1 WHO. WHO coronavirus disease (COVID-19) dashboard. <https://covid19.who.int/> (accessed Jan 26, 2021).
- 2 Yi C, Sun X, Ye J, et al. Key residues of the receptor binding motif in the spike protein of SARS-CoV-2 that interact with ACE2 and neutralizing antibodies. *Cell Mol Immunol* 2020; **17**: 621-30.
- 3 Weisblum Y, Schmidt F, Zhang F, et al. Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants. *Elife* 2020; **9**: e61312.
- 4 Greaney AJ, Starr TN, Gilchuk P, et al. Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition. *Cell Host Microbe* 2021; **29**: 44-57.e9.
- 5 Tegally H, Wilkinson E, Giovanetti M, et al. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *medRxiv* 2020; published online Dec 22. <https://doi.org/10.1101/2020.12.21.20248640> (preprint).

## Estimates of anti-SARS-CoV-2 antibody seroprevalence in Iran

Iran was among the first countries outside China to report a large outbreak of COVID-19, but the transmission dynamics across the country have largely remained unknown due to the scarcity of serological, epidemiological, and genomic data. One of the main barriers

For CovMT see <https://www.cbrc.kaust.edu.sa/covmt>

See Online for appendix

For GISAID see <http://gisaid.org>



Published Online  
February 15, 2021  
[http://dx.doi.org/10.1016/S1473-3099\(21\)00053-0](http://dx.doi.org/10.1016/S1473-3099(21)00053-0)